

# SEQUENCE LISTING

<110> Altboum, Zeev  
Barry, Eileen M.  
Levine, Myron M.

University of Maryland

<120> ISOLATION AND CHARACTERIZATION OF THE  
CSA OPERON

<130> UOFMD.006A

<150> 60/198,626

<151> 2000-04-20

<160> 40

<170> FastSEQ for Windows Version 4.0

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Ala Asn Ala Asn Phe Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn	
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gga aat agc gag tta att cgt gtt tat tca aaa tca aaa gag ata caa	144
Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln	
35 40 45	
tat ata aaa ata tat aca aaa aag att att aat ccc ggc aca act gaa	192
Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu	
50 55 60	
gaa cat gaa gtt gat atg ccc aat tgg gat ggt ggg ttt gta gtt act	240
Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr	
65 70 75 80	
cct caa aaa gtt att ctt cct gca gga ggg agt aaa tca ata cgt tta	288
Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu	
85 90 95	
act caa ttt aga ata cca aaa aaa gag gaa att tat aga gta tat ttt	336
Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe	
100 105 110	
gag gcg gta aaa cca gat agc aaa gaa aat gta att gat aat aaa aaa	384
Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys	
115 120 125	

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# SEQUENCE LISTING

<110> Altboum, Zeev  
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<120> ISOLATION AND CHARACTERIZATION OF THE  
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<130> UOFMD.006A

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cct	caa	aaa	gtt	att	ctt	cct	gca	gga	ggg	agt	aaa	tca	ata	cgt	tta	288
Pro	Gln	Lys	Val	Ile	Leu	Pro	Ala	Gly	Gly	Ser	Lys	Ser	Ile	Arg	Leu	
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 gag gcg gta aaa cca gat agc aaa gaa aat gta att gat aat aaa aaa 384  
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 cta aca aca gag cta tct gtt aat ata att tat gcg gct cta atc aga 432  
 Leu Thr Thr Glu Leu Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg  
 130 135 140  
 tct tta cca agt gaa caa aac ata tca cta aac att tct aga aat gca 480  
 Ser Leu Pro Ser Glu Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala  
 145 150 155 160  
 aga aaa aat ata att att tat aat aat ggg aat gtt aga gca ggt gtt 528  
 Arg Lys Asn Ile Ile Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val  
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 aaa gat att tat ttt tgt aag tca tct aat atc gat gat agc tgt gta 576  
 Lys Asp Ile Tyr Phe Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val  
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 Lys Lys Thr His Asn Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr  
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 Leu Val Asn Asn Asn Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu  
 210 215 220  
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 Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln  
 35 40 45  
 Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu  
 50 55 60  
 Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr  
 65 70 75 80  
 Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu



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Ser	Gly	Val	Thr	Gly	Val	Ser	Ser	Ser	Gln	Asp	Leu	Val	Ile	Gly	Ala	
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 Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu  
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 Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn  
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 Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp  
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 Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu  
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 Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr  
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Ser	Pro	Glu	Ser	Ile	Leu	Asp	Lys	Ile	Asn	Val	Lys	Lys	Glu	Lys	Glu	
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Lys	Lys	Leu	Ser	Val	Leu	Phe	Thr	Asn	Ser	Phe	Ser	Arg	Asn	Gly	Asn	
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atg	agt	tgt	cag	ggg	aat	gct	act	ata	cag	tat	aac	tgc	aat	tac	att	336
Met	Ser	Cys	Gln	Gly	Asn	Ala	Thr	Ile	Gln	Tyr	Asn	Cys	Asn	Tyr	Ile	
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Lys	Thr	Lys	Ser	Val	Asp	Val	Ile	Val	Asp	Asp	Val	Asp	Asn	Val	Val	
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aac	ctt	ttt	ata	ggg	aat	gaa	ttt	ctg	gat	tct	gaa	gca	cac	aat	gat	432
Asn	Leu	Phe	Ile	Gly	Asn	Glu	Phe	Leu	Asp	Ser	Glu	Ala	His	Asn	Asp	
		130				135					140					
gaa	tat	cat	caa	tta	tca	cga	aat	gta	aaa	aaa	gct	ttt	ata	caa	agc	480
Glu	Tyr	His	Gln	Leu	Ser	Arg	Asn	Val	Lys	Lys	Ala	Phe	Ile	Gln	Ser	
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Gln	Thr	Ile	Asn	Val	Ser	Asp	Ser	Gly	Lys	Tyr	Lys	Ser	Leu	Ser	Val	
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Asn	Trp	Trp	Met	Asn	Tyr	Asn	Lys	Phe	Asn	Gly	Tyr	Ser	Asn	Asn	Glu	
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Tyr	Tyr	Gln	Phe	Gly	Arg	Met	Asp	Arg	Thr	Asp	Leu	Ser	Gln	Ser	Ile	
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Ile	Arg	Thr	Gly	Thr	Thr	Gln	Ser	Tyr	Ile	Lys	Asn	Thr	Asp	Lys	Phe	
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Ile	Ala	Ser	Pro	Val	Thr	Val	Met	Leu	Thr	Asn	Phe	Ser	Arg	Val	Glu	
		275					280					285				
gct	ttt	cgc	aat	aat	caa	tta	ttg	ggc	gta	tgg	tat	tta	gat	tct	gga	912
Ala	Phe	Arg	Asn	Asn	Gln	Leu	Leu	Gly	Val	Trp	Tyr	Leu	Asp	Ser	Gly	
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Val	Asn	Glu	Leu	Asp	Thr	Ala	Arg	Leu	Pro	Tyr	Gly	Ser	Tyr	Asp	Leu	
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Lys	Leu	Lys	Ile	Phe	Glu	Asn	Thr	Gln	Leu	Val	Arg	Glu	Glu	Ile	Ile	
				325					330					335		
cct	ttt	aat	aaa	ggg	aga	agt	tct	att	ggc	gat	atg	caa	tgg	gac	gtt	1056
Pro	Phe	Asn	Lys	Gly	Arg	Ser	Ser	Ile	Gly	Asp	Met	Gln	Trp	Asp	Val	
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Phe	Ile	Gln	Gly	Gly	Asn	Ile	Ile	Asn	Asp	Lys	Asp	Arg	Tyr	Ile	Glu	
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aaa	aat	tat	tat	gaa	ggg	agt	ctc	aaa	tgg	aat	tcc	ggc	att	ctg	tct	1248
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Gly Ser Leu Asn Ser Glu Phe Ser Phe Leu Trp Gly Asp Asn Ala Lys	
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ggt aat tat caa agt atc tcg tat acc gat gga ttt agt tta tca ttt	1344
Gly Asn Tyr Gln Ser Ile Ser Tyr Thr Asp Gly Phe Ser Leu Ser Phe	
435 440 445	
tat cat aat gat aag cgg gtc gat aat tgt gga aga aat tac aat gct	1392
Tyr His Asn Asp Lys Arg Val Asp Asn Cys Gly Arg Asn Tyr Asn Ala	
450 455 460	
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Gly Trp Ser Gly Cys Tyr Glu Ser Tyr Ser Ala Ser Leu Ser Ile Pro	
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tta ttg gga tgg aca agt act ctg gga tat agt gac act tat agt gaa	1488
Leu Leu Gly Trp Thr Ser Thr Leu Gly Tyr Ser Asp Thr Tyr Ser Glu	
485 490 495	
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Ser Val Tyr Lys Asn His Ile Leu Ser Glu Tyr Gly Phe Tyr Asn Gln	
500 505 510	
aac ata tat aaa ggg aga acc caa aga tgg caa ctg act tcg tcc acc	1584
Asn Ile Tyr Lys Gly Arg Thr Gln Arg Trp Gln Leu Thr Ser Ser Thr	
515 520 525	
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Ser Leu Lys Trp Met Asp Tyr Asn Phe Met Pro Ala Ile Gly Ile Tyr	
530 535 540	
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565 570 575	
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625 630 635 640	

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Ser Ser Phe Ala Leu Thr Ser Asp Gly Phe Tyr Trp Gly Gly Ser Ala	
660 665 670	
tct ggt ttg aca aaa cta gct ggc ggt att atc aag gtt aaa tca aac	2064
Ser Gly Leu Thr Lys Leu Ala Gly Gly Ile Ile Lys Val Lys Ser Asn	
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Asp Thr Lys Lys Asn Leu Val Lys Val Thr Gly Ala Leu Tyr Gly Asp	
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Tyr Ser Leu Gly Ser Asn Asp Asn Ala Phe Ile Pro Val Pro Ala Leu	
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725 730 735	
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Ile Ser Val Leu Ala Pro Thr Asn Asn Asp Met Phe Ile Leu Pro Gly	
740 745 750	
aat gtt tat cct gtt gaa att gaa acc aaa gta agt gtt tct tat att	2304
Asn Val Tyr Pro Val Glu Ile Glu Thr Lys Val Ser Val Ser Tyr Ile	
755 760 765	
ggt aga ggt ttt gac aaa aac ggc acg cca ctt tct ggc gca cat gtt	2352
Gly Arg Gly Phe Asp Lys Asn Gly Thr Pro Leu Ser Gly Ala His Val	
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Ile Tyr Thr Cys Gln Leu Gly Lys Asn Lys Val His Lys Gly Ile Val	
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ttc gtc gga gat gtt ata tgt gat gtt aat agc aca agt tcc tta cca	2544
Phe Val Gly Asp Val Ile Cys Asp Val Asn Ser Thr Ser Ser Leu Pro	
835 840 845	
gat gaa ttt gta aag aac cca cgt gtg cag gat ttg ctg gca aag aat	2592
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850

855

860

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2604

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Lys	Thr	Lys	Ser	Val	Asp	Val	Ile	Val	Asp	Asp	Val	Asp	Asn	Val	Val
		115					120						125		
Asn	Leu	Phe	Ile	Gly	Asn	Glu	Phe	Leu	Asp	Ser	Glu	Ala	His	Asn	Asp
		130				135						140			
Glu	Tyr	His	Gln	Leu	Ser	Arg	Asn	Val	Lys	Lys	Ala	Phe	Ile	Gln	Ser
145					150					155					160
Gln	Thr	Ile	Asn	Val	Ser	Asp	Ser	Gly	Lys	Tyr	Lys	Ser	Leu	Ser	Val
				165					170					175	
Ser	Gly	Asn	Ser	Ala	Leu	Gly	Ile	Thr	Asp	Thr	Ser	Tyr	Ala	Val	Leu
			180					185					190		
Asn	Trp	Trp	Met	Asn	Tyr	Asn	Lys	Phe	Asn	Gly	Tyr	Ser	Asn	Asn	Glu
	195					200						205			
Arg	Thr	Ile	Asn	Ser	Leu	Tyr	Phe	Arg	His	Asp	Leu	Asp	Lys	Arg	Tyr
	210					215					220				
Tyr	Tyr	Gln	Phe	Gly	Arg	Met	Asp	Arg	Thr	Asp	Leu	Ser	Gln	Ser	Ile
225					230					235					240
Ser	Gly	Asn	Phe	Asn	Phe	Asn	Leu	Leu	Pro	Leu	Pro	Asp	Ile	Asp	Gly
				245					250					255	
Ile	Arg	Thr	Gly	Thr	Thr	Gln	Ser	Tyr	Ile	Lys	Asn	Thr	Asp	Lys	Phe
			260					265					270		
Ile	Ala	Ser	Pro	Val	Thr	Val	Met	Leu	Thr	Asn	Phe	Ser	Arg	Val	Glu
		275					280					285			
Ala	Phe	Arg	Asn	Asn	Gln	Leu	Leu	Gly	Val	Trp	Tyr	Leu	Asp	Ser	Gly
	290					295					300				
Val	Asn	Glu	Leu	Asp	Thr	Ala	Arg	Leu	Pro	Tyr	Gly	Ser	Tyr	Asp	Leu
305					310					315					320
Lys	Leu	Lys	Ile	Phe	Glu	Asn	Thr	Gln	Leu	Val	Arg	Glu	Glu	Ile	Ile
				325					330					335	

00000000000000000000000000000000

770                      775                      780  
 Leu Asn Glu Pro His Val Ile Leu Asp Glu Asp Gly Gly Phe Ser Phe  
 785                      790                      795                      800  
 Glu Tyr Thr Gly Asn Glu Lys Thr Leu Phe Leu Leu Lys Gly Arg Thr  
                     805                      810                      815  
 Ile Tyr Thr Cys Gln Leu Gly Lys Asn Lys Val His Lys Gly Ile Val  
                     820                      825                      830  
 Phe Val Gly Asp Val Ile Cys Asp Val Asn Ser Thr Ser Ser Leu Pro  
                     835                      840                      845  
 Asp Glu Phe Val Lys Asn Pro Arg Val Gln Asp Leu Leu Ala Lys Asn  
                     850                      855                      860  
 Asp Lys Gly  
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 <211> 330  
 <212> DNA  
 <213> E. coli

<220>  
 <221> CDS  
 <222> (1) ... (330)

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 Ile Ser Lys Leu Ala Ala Ser Pro Val Phe Leu Glu Arg Gly Val Asn  
   1                    5                    10                    15  
  
 ata tct gta aga ata cag aag caa att tta tca gaa aaa cca tat gtt 96  
 Ile Ser Val Arg Ile Gln Lys Gln Ile Leu Ser Glu Lys Pro Tyr Val  
                     20                    25                    30  
  
 gca ttc aga ttg aac gga gac ata cta aga cat tta aag gat gca ttg 144  
 Ala Phe Arg Leu Asn Gly Asp Ile Leu Arg His Leu Lys Asp Ala Leu  
                     35                    40                    45  
  
 atg ata ata tat ggt atg tca aaa ata gat acc aat gat tgt aga aat 192  
 Met Ile Ile Tyr Gly Met Ser Lys Ile Asp Thr Asn Asp Cys Arg Asn  
   50                    55                    60  
  
 atg tca agg aaa ata atg aaa aca gaa gtg gat aaa acc tta ctg gat 240  
 Met Ser Arg Lys Ile Met Lys Thr Glu Val Asp Lys Thr Leu Leu Asp  
   65                    70                    75                    80  
  
 gta tta aaa aat ata aat agc tat gat gac tca gct ttt ata tct aat 288  
 Val Leu Lys Asn Ile Asn Ser Tyr Asp Asp Ser Ala Phe Ile Ser Asn  
                     85                    90                    95  
  
 ttg ata tat tta att tca aag atc gag aat aat aaa aaa taa 330  
 Leu Ile Tyr Leu Ile Ser Lys Ile Glu Asn Asn Lys Lys \*  
                     100                    105

<210> 8  
 <211> 109  
 <212> PRT  
 <213> E. coli

<400> 8  
 Ile Ser Lys Leu Ala Ala Ser Pro Val Phe Leu Glu Arg Gly Val Asn  
 1 5 10 15  
 Ile Ser Val Arg Ile Gln Lys Gln Ile Leu Ser Glu Lys Pro Tyr Val  
 20 25 30  
 Ala Phe Arg Leu Asn Gly Asp Ile Leu Arg His Leu Lys Asp Ala Leu  
 35 40 45  
 Met Ile Ile Tyr Gly Met Ser Lys Ile Asp Thr Asn Asp Cys Arg Asn  
 50 55 60  
 Met Ser Arg Lys Ile Met Lys Thr Glu Val Asp Lys Thr Leu Leu Asp  
 65 70 75 80  
 Val Leu Lys Asn Ile Asn Ser Tyr Asp Asp Ser Ala Phe Ile Ser Asn  
 85 90 95  
 Leu Ile Tyr Leu Ile Ser Lys Ile Glu Asn Asn Lys Lys  
 100 105

<210> 9  
 <211> 1086  
 <212> DNA  
 <213> E. coli

<220>  
 <221> CDS  
 <222> (1)...(1086)

<400> 9  
 atg aat aag att tta ttt att ttt aca ttg ttt ttc tct tca gta ctt 48  
 Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu  
 1 5 10 15  
 ttt aca ttt gct gta tcg gca gat aaa att ccc gga gat gaa agc ata 96  
 Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile  
 20 25 30  
 act aat att ttt ggc ccg cgt gac agg aac gaa tct tcc ccc aaa cat 144  
 Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His  
 35 40 45  
 aat ata tta aat aac cat att aca gca tac agt gaa agt cat act ctg 192  
 Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu  
 50 55 60  
 tat gat agg atg act ttt tta tgt ttg tct tct cac aat aca ctt aat 240  
 Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn  
 65 70 75 80  
 gga gca tgt cca acc agt gag aat cct agc agt tca tcg gtc agc ggt 288  
 Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly  
 85 90 95

100-368611-100

305		310		315		320	
atc agt gtt ccg gtg ttg tgt tgg cct gga cgt ttg caa ttg gat gca							1008
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala							
	325			330		335	
aaa gtg gaa aat ccc gag gct gga caa tat atg ggt aat att aat gtt							1056
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val							
	340			345		350	
act ttc aca cca agt agt caa aca ctc tag							1086
Thr Phe Thr Pro Ser Ser Gln Thr Leu *							
	355			360			

<210> 10  
 <211> 361  
 <212> PRT  
 <213> E. coli

<400> 10

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu																			
1				5				10						15					
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile								20				25		30					
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His								35				40		45					
Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu								50				55		60					
Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn								65				70		75				80	
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly								85				90						95	
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys								100				105						110	
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val								115				120						125	
Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn								130				135		140					
Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly								145				150		155				160	
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys								165				170						175	
Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile								180				185						190	
Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu								195				200						205	
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr								210				215		220					
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr								225				230		235				240	
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp								245				250						255	
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp								260				265						270	



Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
           275                                  280                                  285  
 Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala  
           290                                  295                                  300  
 Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu  
 305                                  310                                  315                                  320  
 Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala  
                                   325                                  330                                  335  
 Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val  
                                   340                                  345                                  350  
 Thr Phe Thr Pro Ser Ser Gln Thr Leu  
           355                                  360

<210> 11  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 11  
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<210> 12  
 <211> 30  
 <212> DNA  
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<220>  
 <223> PCR Primer

<400> 12  
 cgacccact ataattcccg ccgttggtgc 30

<210> 13  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 13  
 gtgatatggt ttgttcactt ggtaaagatc 30

<210> 14  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 14  
 ctcatggctc catttggtgc aaatgcaaac tttatg 36  
  
 <210> 15  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
 <400> 15  
 gggatcgatc ccggggcggc cgcgggcccg gtaccaggcc ttctagaaag cttgacgtcg 60  
  
 <210> 16  
 <211> 61  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
 <400> 16  
 cccgctagcg gcgcgcctcg cgaggatccg tcgacgacgt caagctttct agaaggcctg 60  
 g 61  
  
 <210> 17  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
 <400> 17  
 aagcttgacg tcgtcgacgg 20  
  
 <210> 18  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
 <400> 18  
 cccgctagcg gcgcgcctcg cg 22  
  
 <210> 19  
 <211> 26  
 <212> DNA  
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 <220>

<223> PCR Primer

<400> 19

ccgtgctgac tctacacccc cagatg

26

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 20

gcacatagag aggatagtaa cgccg

25

<210> 21

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 21

cggtcattgt tggccgtgcg ctgcc

25

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 22

cacgcagcgc gctgatgcct tccacgcg

28

<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 23

catatttgat atctgagata tctgg

25

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 24

tgttgcattc agattgaacg gag

23

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 25

tattatgatt cataaataca ctgt

24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

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<400> 26

tgtaggtatt tgtaggtgaca tcgcagcatt aaatataaaa atagcacagg

50

<210> 27

<211> 7239

<212> DNA

<213> E. coli

<220>

<221> CDS

<222> (283) ... (999)

<221> CDS

<222> (1028) ... (1531)

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<400> 27

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gtctggaaat cgcaggacca agaactctca gtacatctgt ggcgataata ttatcgcttc 120  
ttatacattc caatatgcag ttcttgtggg tatttgtttg gacatcgag cattaaatat 180  
aaaaatagca caggaggcat aattatttgt ttttactgtc ttattttttt atcccathtt 240  
tttttgtttt gatttatctt tgatgaaagc tcaggaggga atatg cat aaa tta ttt 297

His Lys Leu Phe

tgt tta cta agt tta ctc ata act cca ttt gtt gca aat gca aac ttt	345
Cys Leu Leu Ser Leu Leu Ile Thr Pro Phe Val Ala Asn Ala Asn Phe	
5 10 15 20	
atg ata tat cca ata tca aaa gat tta aag aat gga aat agc gag tta	393
Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn Gly Asn Ser Glu Leu	
25 30 35	
att cgt gtt tat tca aaa tca aaa gag ata caa tat ata aaa ata tat	441
Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln Tyr Ile Lys Ile Tyr	
40 45 50	
aca aaa aag att att aat ccc ggc aca act gaa gaa cat gaa gtt gat	489
Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu Glu His Glu Val Asp	
55 60 65	
atg ccc aat tgg gat ggt ggg ttt gta gtt act cct caa aaa gtt att	537
Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr Pro Gln Lys Val Ile	
70 75 80	
ctt cct gca gga ggg agt aaa tca ata cgt tta act caa ttt aga ata	585
Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu Thr Gln Phe Arg Ile	
85 90 95 100	
cca aaa aaa gag gaa att tat aga gta tat ttt gag gcg gta aaa cca	633
Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe Glu Ala Val Lys Pro	
105 110 115	
gat agc aaa gaa aat gta att gat aat aaa aaa cta aca aca gag cta	681
Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys Leu Thr Thr Glu Leu	
120 125 130	
tct gtt aat ata att tat gcg gct cta atc aga tct tta cca agt gaa	729
Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg Ser Leu Pro Ser Glu	
135 140 145	
caa aac ata tca cta aac att tct aga aat gca aga aaa aat ata att	777
Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala Arg Lys Asn Ile Ile	
150 155 160	
att tat aat aat ggg aat gtt aga gca ggt gtt aaa gat att tat ttt	825
Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val Lys Asp Ile Tyr Phe	
165 170 175 180	
tgt aag tca tct aat atc gat gat agc tgt gta aaa aaa acg cat aac	873
Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val Lys Lys Thr His Asn	
185 190 195	
aag aat ata tat cca gaa aag tca ttt gat acg ctg gtt aat aac aat	921
Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr Leu Val Asn Asn Asn	
200 205 210	
ttt tct tat gtt ttc att aaa tta aac cat gaa gac ata gaa aaa gag	969

Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu Asp Ile Glu Lys Glu  
215 220 225  
  
caa gga cta ata caa tta aaa gtt cct tga tta ctcatctata tactaaggag 1022  
Gln Gly Leu Ile Gln Leu Lys Val Pro \* Leu  
230 235  
  
ttctaatagaa attaaaaaaaa actattgggtg caatg gca ctg acc aca atg ttt 1075  
Ala Leu Thr Thr Met Phe  
240  
  
gta gct atg agt gct tct gca gta gag aaa aat atc act gta aca gct 1123  
Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala  
245 250 255 260  
  
agt gtt gat cct aca att gat att ttg caa gct gat ggt agt agt tta 1171  
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu  
265 270 275  
  
cct act gct gta gaa tta acc tat tca cct gcg gca agt cgt ttt gaa 1219  
Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu  
280 285 290  
  
aat tat aaa atc gca act aaa gtt cat aca aat gtt ata aat aaa aat 1267  
Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn  
295 300 305  
  
gta cta gtt aag ctt gta aat gat cca aaa ctt aca aat gtt ttg gat 1315  
Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp  
310 315 320  
  
tct aca aaa caa ctc ccc att act gta tca tat gga gga aag act cta 1363  
Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu  
325 330 335 340  
  
tca acc gca gat gtg act ttt gaa cct gca gaa tta aat ttt gga acg 1411  
Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr  
345 350 355  
  
tca ggt gta act ggt gta tct tct tcc caa gat tta gtg att ggt gcg 1459  
Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala  
360 365 370  
  
act aca gca caa gca cca acg gcg gga aat tat agt ggg gtc gtt tct 1507  
Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser  
375 380 385  
  
atc tta atg acc tta gca tca taa ata ttttaatatata taaaggagca 1554  
Ile Leu Met Thr Leu Ala Ser \* Ile  
390 395  
  
ggcacactgc tccttattat atggcaataa taaaatg aca aaa aaa aat aca tta 1609  
Thr Lys Lys Asn Thr Leu  
400

tat ata acg atc atc gca atg cta act cca tat tca gtt ttt tcc gga	1657
Tyr Ile Thr Ile Ile Ala Met Leu Thr Pro Tyr Ser Val Phe Ser Gly	
405 410 415	
gat ata ccc aac tct ttc cgt gat tta tgg gga gaa caa gat gaa ttt	1705
Asp Ile Pro Asn Ser Phe Arg Asp Leu Trp Gly Glu Gln Asp Glu Phe	
420 425 430	
tat gaa gta aaa cta tat gga caa act cta gga ata cat cga att aaa	1753
Tyr Glu Val Lys Leu Tyr Gly Gln Thr Leu Gly Ile His Arg Ile Lys	
435 440 445 450	
aca acc cca aca cat att aag ttt tat tca ccc gaa agc att tta gat	1801
Thr Thr Pro Thr His Ile Lys Phe Tyr Ser Pro Glu Ser Ile Leu Asp	
455 460 465	
aaa ata aat gta aaa aaa gaa aag gaa aag aaa ttg agt gtt ttg ttc	1849
Lys Ile Asn Val Lys Lys Glu Lys Glu Lys Lys Leu Ser Val Leu Phe	
470 475 480	
act aat tct ttt tca aga aat ggc aat atg agt tgt cag ggg aat gct	1897
Thr Asn Ser Phe Ser Arg Asn Gly Asn Met Ser Cys Gln Gly Asn Ala	
485 490 495	
act ata cag tat aac tgc aat tac att aaa aca aaa tca gta gat gtc	1945
Thr Ile Gln Tyr Asn Cys Asn Tyr Ile Lys Thr Lys Ser Val Asp Val	
500 505 510	
atc gtt gat gat gtt gat aat gtt gtt aac ctt ttt ata ggt aat gaa	1993
Ile Val Asp Asp Val Asp Asn Val Val Asn Leu Phe Ile Gly Asn Glu	
515 520 525 530	
ttt ctg gat tct gaa gca cac aat gat gaa tat cat caa tta tca cga	2041
Phe Leu Asp Ser Glu Ala His Asn Asp Glu Tyr His Gln Leu Ser Arg	
535 540 545	
aat gta aaa aaa gct ttt ata caa agc cag aca att aat gtc tca gat	2089
Asn Val Lys Lys Ala Phe Ile Gln Ser Gln Thr Ile Asn Val Ser Asp	
550 555 560	
tct ggg aag tat aaa agt ttg tct gtt tca ggg aat agc gcg ctg ggt	2137
Ser Gly Lys Tyr Lys Ser Leu Ser Val Ser Gly Asn Ser Ala Leu Gly	
565 570 575	
att aca gat aca agt tat gct gtc tta aat tgg tgg atg aat tac aat	2185
Ile Thr Asp Thr Ser Tyr Ala Val Leu Asn Trp Trp Met Asn Tyr Asn	
580 585 590	
aaa ttt aat ggt tac agc aac aac gaa aga aca atc aat agt ttg tac	2233
Lys Phe Asn Gly Tyr Ser Asn Asn Glu Arg Thr Ile Asn Ser Leu Tyr	
595 600 605 610	
ttt aga cat gat tta gat aag aga tat tat tat caa ttt gga cga atg	2281
Phe Arg His Asp Leu Asp Lys Arg Tyr Tyr Tyr Gln Phe Gly Arg Met	
615 620 625	

gat cgt aca gat ttg tca caa agt att agc ggg aac ttt aat ttt aac	2329
Asp Arg Thr Asp Leu Ser Gln Ser Ile Ser Gly Asn Phe Asn Phe Asn	
630 635 640	
tta ctt cct tta ccc gat att gat ggt ata agg aca gga acc aca caa	2377
Leu Leu Pro Leu Pro Asp Ile Asp Gly Ile Arg Thr Gly Thr Thr Gln	
645 650 655	
tct tat atc aaa aat aca gat aag ttt atc gca tcc cct gta act gtt	2425
Ser Tyr Ile Lys Asn Thr Asp Lys Phe Ile Ala Ser Pro Val Thr Val	
660 665 670	
atg tta act aat ttt tcc aga gtg gaa gct ttt cgc aat aat caa tta	2473
Met Leu Thr Asn Phe Ser Arg Val Glu Ala Phe Arg Asn Asn Gln Leu	
675 680 685 690	
ttg ggc gta tgg tat tta gat tct gga gta aat gaa tta gat aca gct	2521
Leu Gly Val Trp Tyr Leu Asp Ser Gly Val Asn Glu Leu Asp Thr Ala	
695 700 705	
cgt tta cct tat ggt agt tac gat ctt aaa tta aaa att ttt gaa aat	2569
Arg Leu Pro Tyr Gly Ser Tyr Asp Leu Lys Leu Lys Ile Phe Glu Asn	
710 715 720	
act cag tta gtt cgt gaa gaa ata att cct ttt aat aaa ggg aga agt	2617
Thr Gln Leu Val Arg Glu Glu Ile Ile Pro Phe Asn Lys Gly Arg Ser	
725 730 735	
tct att ggt gat atg caa tgg gac gtt ttc att cag gga ggg aat att	2665
Ser Ile Gly Asp Met Gln Trp Asp Val Phe Ile Gln Gly Gly Asn Ile	
740 745 750	
att aat gac aag gat cgt tac ata gaa aaa caa aat aat cat aag tca	2713
Ile Asn Asp Lys Asp Arg Tyr Ile Glu Lys Gln Asn Asn His Lys Ser	
755 760 765 770	
tca gtt aat gct ggg cta cgt tta cca att acg aaa aat atc tct gtt	2761
Ser Val Asn Ala Gly Leu Arg Leu Pro Ile Thr Lys Asn Ile Ser Val	
775 780 785	
caa caa gga gca tct gtt ata gat aat aaa aat tat tat gaa ggg agt	2809
Gln Gln Gly Ala Ser Val Ile Asp Asn Lys Asn Tyr Tyr Glu Gly Ser	
790 795 800	
ctc aaa tgg aat tcc ggc att ctg tct ggc tca cta aat agt gag ttc	2857
Leu Lys Trp Asn Ser Gly Ile Leu Ser Gly Ser Leu Asn Ser Glu Phe	
805 810 815	
agt ttt ctt tgg gga gat aat gca aaa ggt aat tat caa agt atc tcg	2905
Ser Phe Leu Trp Gly Asp Asn Ala Lys Gly Asn Tyr Gln Ser Ile Ser	
820 825 830	
tat acc gat gga ttt agt tta tca ttt tat cat aat gat aag cgg gtc	2953
Tyr Thr Asp Gly Phe Ser Leu Ser Phe Tyr His Asn Asp Lys Arg Val	



835		840		845		850	
gat aat tgt gga aga aat tac aat gct ggt tgg agt gga tgc tac gaa	3001						
Asp Asn Cys Gly Arg Asn Tyr Asn Ala Gly Trp Ser Gly Cys Tyr Glu							
		855		860		865	
tca tat tcg gca tct tta agt att cct tta ttg gga tgg aca agt act	3049						
Ser Tyr Ser Ala Ser Leu Ser Ile Pro Leu Leu Gly Trp Thr Ser Thr							
		870		875		880	
ctg gga tat agt gac act tat agt gaa tca gtt tat aaa aac cat att	3097						
Leu Gly Tyr Ser Asp Thr Tyr Ser Glu Ser Val Tyr Lys Asn His Ile							
		885		890		895	
ctt tct gaa tat ggt ttt tat aat caa aac ata tat aaa ggg aga acc	3145						
Leu Ser Glu Tyr Gly Phe Tyr Asn Gln Asn Ile Tyr Lys Gly Arg Thr							
		900		905		910	
caa aga tgg caa ctg act tcg tcc acc tct tta aaa tgg atg gat tat	3193						
Gln Arg Trp Gln Leu Thr Ser Ser Thr Ser Leu Lys Trp Met Asp Tyr							
		915		920		925	930
aat ttt atg cca gca att gga ata tat aac agt gag caa aga caa ctg	3241						
Asn Phe Met Pro Ala Ile Gly Ile Tyr Asn Ser Glu Gln Arg Gln Leu							
		935		940		945	
act gat aaa ggc gga tat ata tct gta act ctc acc cga gcc agc aga	3289						
Thr Asp Lys Gly Gly Tyr Ile Ser Val Thr Leu Thr Arg Ala Ser Arg							
		950		955		960	
gaa aat tca tta aac gca ggg tat tct tac aac tat tcc aga gga aag	3337						
Glu Asn Ser Leu Asn Ala Gly Tyr Ser Tyr Asn Tyr Ser Arg Gly Lys							
		965		970		975	
tat tct tct aac gaa tta ttt gtt gat gga tat atg aca tca aca aat	3385						
Tyr Ser Ser Asn Glu Leu Phe Val Asp Gly Tyr Met Thr Ser Thr Asn							
		980		985		990	
aat ggt gac tat cat gag gta aga atg cgt ttt aat aaa aat aga cat	3433						
Asn Gly Asp Tyr His Glu Val Arg Met Arg Phe Asn Lys Asn Arg His							
		995		1000		1005	1010
aat gca gaa ggt aga ctt tca ggt cgt ata aac aat cga ttt gga gat	3481						
Asn Ala Glu Gly Arg Leu Ser Gly Arg Ile Asn Asn Arg Phe Gly Asp							
		1015		1020		1025	
tta aat ggt tca ttc agc atg aat aaa aac aga aac acc aac agt agc	3529						
Leu Asn Gly Ser Phe Ser Met Asn Lys Asn Arg Asn Thr Asn Ser Ser							
		1030		1035		1040	
aat cat tct ctc act ggt ggt tat aat tcc tca ttt gct ctt aca agt	3577						
Asn His Ser Leu Thr Gly Gly Tyr Asn Ser Ser Phe Ala Leu Thr Ser							
		1045		1050		1055	
gat gga ttt tac tgg gga gga agt gca tct ggt ttg aca aaa cta gct	3625						

Asp Gly Phe Tyr Trp Gly Gly Ser Ala Ser Gly Leu Thr Lys Leu Ala	
1060	1065 1070
ggc ggt att atc aag gtt aaa tca aac gat act aaa aaa aat ctg gta	3673
Gly Gly Ile Ile Lys Val Lys Ser Asn Asp Thr Lys Lys Asn Leu Val	
1075	1080 1085 1090
aaa gtg act ggg gca ttg tac ggt gat tat tcg cta ggg agc aac gat	3721
Lys Val Thr Gly Ala Leu Tyr Gly Asp Tyr Ser Leu Gly Ser Asn Asp	
	1095 1100 1105
aat gct ttt att cct gta cca gca tta act cca gcc agt tta att att	3769
Asn Ala Phe Ile Pro Val Pro Ala Leu Thr Pro Ala Ser Leu Ile Ile	
	1110 1115 1120
gaa gat aat aat tat ggt gac aag aat att tct gta ctt gca cca acg	3817
Glu Asp Asn Asn Tyr Gly Asp Lys Asn Ile Ser Val Leu Ala Pro Thr	
	1125 1130 1135
aac aac gat atg ttt ata ttg ccg ggt aat gtt tat cct gtt gaa att	3865
Asn Asn Asp Met Phe Ile Leu Pro Gly Asn Val Tyr Pro Val Glu Ile	
	1140 1145 1150
gaa acc aaa gta agt gtt tct tat att ggt aga ggt ttt gac aaa aac	3913
Glu Thr Lys Val Ser Val Ser Tyr Ile Gly Arg Gly Phe Asp Lys Asn	
	1155 1160 1165 1170
ggc acg cca ctt tct ggc gca cat gtt ttg aat gaa cca cat gtt atc	3961
Gly Thr Pro Leu Ser Gly Ala His Val Leu Asn Glu Pro His Val Ile	
	1175 1180 1185
ctg gat gag gac ggt gga ttt tcg ttt gaa tat aca ggt aat gag aaa	4009
Leu Asp Glu Asp Gly Gly Phe Ser Phe Glu Tyr Thr Gly Asn Glu Lys	
	1190 1195 1200
aca ctt ttt tta tta aag ggc aga act att tat aca tgt caa ctg ggg	4057
Thr Leu Phe Leu Leu Lys Gly Arg Thr Ile Tyr Thr Cys Gln Leu Gly	
	1205 1210 1215
aaa aat aaa gtt cac aaa ggc att gtt ttc gtc gga gat gtt ata tgt	4105
Lys Asn Lys Val His Lys Gly Ile Val Phe Val Gly Asp Val Ile Cys	
	1220 1225 1230
gat gtt aat agc aca agt tcc tta cca gat gaa ttt gta aag aac cca	4153
Asp Val Asn Ser Thr Ser Ser Leu Pro Asp Glu Phe Val Lys Asn Pro	
	1235 1240 1245 1250
cgt gtg cag gat ttg ctg gca aag aat gat aaa gga taa acg	4195
Arg Val Gln Asp Leu Leu Ala Lys Asn Asp Lys Gly * Thr	
	1255 1260
atg aat aag att tta ttt att ttt aca ttg ttt ttc tct tca gta ctt	4243
Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu	
	1265 1270 1275

ttt aca ttt gct gta tcg gca gat aaa att ccc gga gat gaa agc ata	4291
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile	
1280 1285 1290	
act aat att ttt ggc ccg cgt gac agg aac gaa tct tcc ccc aaa cat	4339
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His	
1295 1300 1305 1310	
aat ata tta aat aac cat att aca gca tac agt gaa agt cat act ctg	4387
Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu	
1315 1320 1325	
tat gat agg atg act ttt tta tgt ttg tct tct cac aat aca ctt aat	4435
Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn	
1330 1335 1340	
gga gca tgt cca acc agt gag aat cct agc agt tca tcg gtc agc ggt	4483
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly	
1345 1350 1355	
gaa aca aat ata aca tta caa ttt acg gaa aaa aga agt tta ata aaa	4531
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys	
1360 1365 1370	
aga gag cta caa att aaa ggc tat aaa caa tta ttg ttc aaa agt gtt	4579
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val	
1375 1380 1385 1390	
aac tgc cca tcc ggc cta aca ctt aac tca gct cat ttt aac tgt aat	4627
Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn	
1395 1400 1405	
aaa aac gcg gct tca ggt gca agt tta tat tta tat att cct gct ggc	4675
Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly	
1410 1415 1420	
gaa cta aaa aat ttg cct ttt ggt ggt atc tgg gat gct act ctg aag	4723
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys	
1425 1430 1435	
tta aga gta aaa aga cga tat agt gag acc tat gga act tac act ata	4771
Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile	
1440 1445 1450	
aat atc act att aaa tta act gat aag gga aat att cag ata tgg tta	4819
Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu	
1455 1460 1465 1470	
cct cag ttc aaa agt gac gct cgc gtc gat ctt aac ttg cgt cca act	4867
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr	
1475 1480 1485	
ggt ggg ggc aca tat att gga aga aat tct gtt gat atg tgc ttt tat	4915
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr	
1490 1495 1500	

gat gga tat agt act aac agc agc tct ttg gag ata aga ttt cag gat 4963  
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
1505 1510 1515

aac aat cct aaa tct gat ggg aaa ttt tat cta agg aaa ata aat gat 5011  
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp  
1520 1525 1530

gac acc aaa gaa att gca tat act ttg tca ctt ctc ttg gcg ggt aaa 5059  
Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
1535 1540 1545 1550

agt tta act cca aca aat gga acg tca tta aat att gct gac gca gct 5107  
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala  
1555 1560 1565

tct ctg gaa aca aac tgg aat aga att aca gct gtc acc atg cca gaa 5155  
Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu  
1570 1575 1580

atc agt gtt ccg gtg ttg tgt tgg cct gga cgt ttg caa ttg gat gca 5203  
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala  
1585 1590 1595

aaa gtg gaa aat ccc gag gct gga caa tat atg ggt aat att aat gtt 5251  
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val  
1600 1605 1610

act ttc aca cca agt agt caa aca ctc tag ata acaacaatat tggcgctatt 5304  
Thr Phe Thr Pro Ser Ser Gln Thr Leu \* Ile  
1615 1620

gcgcgcgaat attgtaaagg ggtaaatctgt ttgttaacaa aacattttgt ttcaattcag 5364  
tttgcacgc aataaatctc tactagagac atttttatac agcatagtat tatacaacac 5424  
attcaaaaata aggatatttt tatccacctt taaaataagt aaaaaactgc tttggtataa 5484  
caccataatg tttattaaaa accctaataa aataagatgt actggaaaatt ccaatcatat 5544  
ttgatattctg agatatctgg tatgaatttt caagtagtaa taacgctgcc ttgctcattc 5604  
tcaattgcat taagaactgg ttaaaattag tattctcaga ttctagtctt tttctgatgg 5664  
ttatttctga ttcattaaac atatctgcaa tgatagccag tgtccatttt ctggatagat 5724  
ctttttcgat aatatttctg accttgtcag aaaaaaattc acagatgata tataaattga 5784  
ttctatta ttt ttt att att ctc gat ctt tga aat taa ata tat caa att 5834  
Phe Phe Ile Ile Leu Asp Leu \* Asn \* Ile Tyr Gln Ile  
1625 1630 1635

aga tat aaa agc tga gtc atc ata gct att tat att ttt taa tac atc 5882  
Arg Tyr Lys Ser \* Val Ile Ile Ala Ile Tyr Ile Phe \* Tyr Ile  
1640 1645 1650

cag taa ggt ttt atc cac ttc tgt ttt cat tat ttt cct tga cat att 5930  
Gln \* Gly Phe Ile His Phe Cys Phe His Tyr Phe Pro \* His Ile  
1655 1660

tct aca atc att ggt atc tat ttt tga cat acc ata tat tat cat caa 5978  
Ser Thr Ile Ile Gly Ile Tyr Phe \* His Thr Ile Tyr Tyr His Gln

1665

1670

1675

tgc atc ctt taa atg tct tag tat gtc tcc gtt caa tct gaa tgc aac 6026  
 Cys Ile Leu \* Met Ser \* Tyr Val Ser Val Gln Ser Glu Cys Asn  
 1680 1685 1690

ata tgg ttt ttc tga taa aat ttg ctt ctg tat tct tac aga tat att 6074  
 Ile Trp Phe Phe \* \* Asn Leu Leu Leu Tyr Ser Tyr Arg Tyr Ile  
 1695 1700 1705

cac ccc tct ttc aag aaa tac agg t gatgctgccca acttactgat 6119  
 His Pro Ser Phe Lys Lys Tyr Arg  
 1710 1715

ttagtgatg atggtgtttt tgagggtgctc cagtggcttc tgtttctatc agctgtccct 6179  
 cctgttcagc tactgacggg gtgggtgcgta acggcaaaag cactgccgga catcagcgct 6239  
 atctctgctc tctactgccgt aaaacatggc aactgcagtt cacttacact gcttctcaac 6299  
 ccggtacgca ccagaaaatc attgatatgg ccatgaatgg cgttggatgc cgggcaacag 6359  
 cccgcattat gggcggtggc ctcaacacga ttttacgtca cttaaaaaac tcaggccgca 6419  
 gtcggtaacc tcgcgcatac agccgggcag tgacgtcatc gtctgcgcgg aaatggacga 6479  
 acagtggggc tatgtcgggg ctaaatacgc ccagcgctgg ctgttttacg cgtatgacag 6539  
 gctccggaag acggttggtg cgcacgtatt cgggtgaacgc actatggcga cgctggggcg 6599  
 tcttatgagc ctgctgtcac cctttgacgt ggtgatatgg atgacggatg gctggccgct 6659  
 gtatgaatcc cgcctgaagg gaaagctgca cgtaatcagc aagcgatata cgcagcgaat 6719  
 tgagcggcat aacctgaatc tgaggcagca cctggcacgg ctgggacgga agtcgctgtc 6779  
 gttctcaaaa tcggtggagc tgcatgacaa agtcacggg cattatctga acataaaaca 6839  
 ctactccgcg gttagagtca ttacctggtt acagtattat tatccgtgac tctttcctgg 6899  
 taactccgcg ataataacct cactttttcca gtattccaga agatgatgtt ttttcctcga 6959  
 taataaaaaat gtgccaatat ggaaataaga aatcggattt tttatcagca tacgcaaatt 7019  
 ttcagataac aatgaataca gatgtatttt atatacacag ataaaaccgc gcaacagaca 7079  
 taaatatgac agtagcatga aaaagcagag agagacaggg tgatacagaa aagtaactat 7139  
 ttttttagct atagtattat tggttttacc tattttcgtg attgtgtttc tgtatatttg 7199  
 acaatgagtc tctcagaatc ggtttctcga agtgacgagc 7239

&lt;210&gt; 28

&lt;211&gt; 361

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ETEC Protein Homology Sequence

&lt;400&gt; 28

Thr Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val  
 1 5 10 15  
 Leu Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser  
 20 25 30  
 Ile Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys  
 35 40 45  
 His Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr  
 50 55 60  
 Leu Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu  
 65 70 75 80  
 Asn Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser  
 85 90 95

Gly	Glu	Thr	Asn	Ile	Thr	Leu	Gln	Phe	Thr	Glu	Lys	Arg	Ser	Leu	Ile
			100					105					110		
Lys	Arg	Glu	Leu	Gln	Ile	Lys	Gly	Tyr	Lys	Gln	Leu	Leu	Phe	Lys	Ser
		115					120					125			
Val	Asn	Cys	Pro	Ser	Gly	Leu	Thr	Leu	Asn	Ser	Ala	His	Phe	Asn	Cys
		130				135					140				
Asn	Lys	Asn	Ala	Ala	Ser	Gly	Ala	Ser	Leu	Tyr	Leu	Tyr	Ile	Pro	Ala
145					150					155					160
Gly	Glu	Leu	Lys	Asn	Leu	Pro	Phe	Gly	Gly	Ile	Trp	Asp	Ala	Thr	Leu
				165					170					175	
Lys	Leu	Arg	Val	Lys	Arg	Arg	Tyr	Ser	Glu	Thr	Tyr	Gly	Thr	Tyr	Thr
			180					185					190		
Ile	Asn	Ile	Thr	Ile	Lys	Leu	Thr	Asp	Lys	Gly	Asn	Ile	Gln	Ile	Trp
		195					200					205			
Leu	Pro	Gln	Phe	Lys	Ser	Asp	Ala	Arg	Val	Asp	Leu	Asn	Leu	Arg	Pro
		210				215					220				
Thr	Gly	Gly	Gly	Thr	Tyr	Ile	Gly	Arg	Asn	Ser	Val	Asp	Met	Cys	Phe
225					230					235					240
Tyr	Asp	Gly	Tyr	Ser	Thr	Asn	Ser	Ser	Ser	Leu	Glu	Ile	Arg	Phe	Gln
				245					250					255	
Asp	Asn	Asn	Pro	Lys	Ser	Asp	Gly	Lys	Phe	Tyr	Leu	Arg	Lys	Ile	Asn
			260					265					270		
Asp	Asp	Thr	Lys	Glu	Ile	Ala	Tyr	Thr	Leu	Ser	Leu	Leu	Leu	Ala	Gly
		275					280					285			
Ser	Leu	Thr	Pro	Thr	Asn	Gly	Thr	Ser	Leu	Asn	Ile	Ala	Asp	Ala	Ala
						295					300				
Ser	Leu	Phe	Thr	Asn	Trp	Asn	Arg	Ile	Thr	Ala	Val	Thr	Met	Pro	Glu
305					310					315					320
Ile	Ser	Val	Pro	Val	Leu	Cys	Trp	Pro	Gly	Arg	Leu	Gln	Leu	Asp	Ala
				325					330					335	
Lys	Val	Glu	Asn	Pro	Glu	Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Asn	Val
			340					345					350		
Thr	Phe	Thr	Pro	Ser	Ser	Gln	Thr	Leu							
		355					360								

<210> 29

&lt;212&gt; PRT

 $\langle 220 \rangle$ 

<400> 29

Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met  
20 25 30

Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu  
50 55 60

Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn  
65 70 75 80

Gly	Ala	Cys	Pro	Ser	Asp	Ala	Pro	Gly	Thr	Ala	Thr	Ile	Asp	Gly		
				85					90					95	Gly	
Glu	Thr	Asn	Ile	Thr	Leu	Gln	Phe	Thr	Glu	Lys	Arg	Ser	Leu	Ile	Lys	
				100					105					110	Lys	
Arg	Glu	Leu	Gln	Ile	Lys	Gly	Tyr	Lys	Gln	Phe	Leu	Phe	Lys	Asn	Ala	
				115					120					125	Ala	
Asn	Cys	Pro	Ser	Lys	Leu	Ala	Leu	Asn	Ser	Ser	His	Phe	Gln	Cys	Asn	
				130					135					140	Asn	
Arg	Glu	Gln	Ala	Ser	Gly	Ala	Thr	Leu	Ser	Leu	Tyr	Ile	Pro	Ala	Gly	
145					150					155					160	Gly
Glu	Leu	Asn	Lys	Leu	Pro	Phe	Gly	Gly	Val	Trp	Asn	Ala	Val	Leu	Lys	
				165					170					175	Lys	
Leu	Asn	Val	Lys	Arg	Arg	Tyr	Thr	Thr	Tyr	Gly	Thr	Tyr	Thr	Ile	Asn	
				180					185					190	Asn	
Ile	Thr	Val	Asn	Leu	Thr	Asp	Lys	Gly	Asn	Ile	Gln	Ile	Trp	Leu	Pro	
				195					200					205	Pro	
Gln	Phe	Lys	Ser	Asn	Ala	Arg	Val	Asp	Leu	Asn	Leu	Arg	Pro	Thr	Gly	
				210					215					220	Gly	
Gly	Gly	Thr	Tyr	Ile	Gly	Arg	Asn	Ser	Val	Asp	Met	Cys	Phe	Tyr	Asp	
225					230					235					240	Asp
Gly	Tyr	Ser	Thr	Met	Ser	Ser	Ser	Leu	Glu	Ile	Arg	Phe	Gln	Asp	Asp	
				245					250					255	Asp	
Asn	Ser	Lys	Ser	Asp	Gly	Lys	Phe	Tyr	Leu	Lys	Lys	Ile	Asn	Asp	Asp	
				260					265					270	Asp	
Ser	Lys	Glu	Leu	Val	Tyr	Thr	Leu	Ser	Leu	Leu	Leu	Ala	Gly	Lys	Asn	
				275					280					285	Asn	
Leu	Thr	Pro	Thr	Asn	Gly	Gln	Ala	Leu	Asn	Ile	Asn	Thr	Ala	Ser	Leu	
				290					295					300	Leu	
Glu	Thr	Asn	Trp	Asn	Arg	Ile	Thr	Ala	Val	Thr	Met	Pro	Glu	Ile	Ser	
305					310					315					320	Ser
Val	Pro	Val	Leu	Cys	Trp	Pro	Gly	Arg	Leu	Gln	Leu	Asp	Ala	Lys	Val	
				325					330					335	Val	
Lys	Asn	Pro	Glu	Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Lys	Ile	Thr	Phe	
				340					345					350	Phe	
Thr	Pro	Ser	Ser	Gln	Thr	Leu										
				355												

<210> 30

&lt;212&gt; PRT

<220>

<400> 30

Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala  
 65 70 75 80  
 Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly  
 85 90 95  
 Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg  
 100 105 110  
 Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp  
 115 120 125  
 Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val  
 130 135 140  
 Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile  
 145 150 155 160  
 Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Lys Ala  
 165 170 175  
 Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr  
 180 185 190  
 Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
 Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu  
 210 215 220  
 Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met  
 225 230 235 240  
 Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg  
 245 250 255  
 Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys  
 260 265 270  
 Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu  
 275 280 285  
 Gly Gly Arg Glu Phe Tyr Pro Asn Asn Gly Lys Ala Phe Thr Ile Asn  
 290 295 300  
 Asp Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser  
 305 310 315 320  
 Leu Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr  
 325 330 335  
 Phe Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile  
 340 345 350  
 Leu Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu  
 355 360

<210> 31

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> ETEC Protein Homology Sequence

<400> 31

Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val  
 1 5 10 15  
 Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser  
 20 25 30  
 Phe Gln Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn  
 35 40 45



Ile	Phe	Thr	Asn	His	Val	Ala	Gly	Tyr	Ser	Leu	Ser	His	Ser	Leu	Tyr
50						55					60				
Asp	Arg	Ile	Val	Phe	Leu	Cys	Thr	Ser	Ser	Ser	Asn	Pro	Val	Asn	Gly
65					70					75					80
Ala	Cys	Pro	Thr	Ile	Gly	Thr	Ser	Gly	Val	Gln	Tyr	Gly	Thr	Thr	Thr
				85					90					95	
Ile	Thr	Leu	Gln	Phe	Thr	Glu	Lys	Arg	Ser	Leu	Ile	Lys	Arg	Asn	Ile
			100					105					110		
Asn	Ile	Ala	Gly	Asn	Lys	Lys	Pro	Ile	Trp	Glu	Asn	Gln	Ser	Cys	Asp
		115					120					125			
Phe	Ser	Asn	Ile	Met	Val	Leu	Asn	Ser	Lys	Ser	Trp	Ser	Cys	Gly	Ala
	130					135					140				
His	Gly	Asn	Ala	Asn	Gly	Thr	Ile	Leu	Asn	Leu	Tyr	Ile	Pro	Ala	Gly
145					150					155					160
Glu	Ile	Asn	Lys	Leu	Pro	Phe	Gly	Gly	Ile	Trp	Glu	Ala	Thr	Leu	Ile
				165					170					175	
Leu	Arg	Leu	Ser	Arg	Tyr	Gly	Glu	Val	Ser	Ser	Thr	His	Tyr	Gly	Asn
			180					185					190		
Tyr	Thr	Val	Asn	Ile	Thr	Val	Asp	Leu	Thr	Asp	Lys	Gly	Asn	Ile	Gln
		195					200					205			
Val	Trp	Leu	Pro	Gly	Phe	His	Ser	Asn	Pro	Arg	Val	Asp	Leu	Asn	Leu
	210					215					220				
Arg	Pro	Ile	Gly	Asn	Tyr	Lys	Tyr	Ser	Gly	Ser	Asn	Ser	Leu	Asp	Met
225					230					235					240
Cys	Phe	Tyr	Asp	Gly	Tyr	Ser	Thr	Asn	Ser	Asp	Ser	Met	Val	Ile	Lys
				245					250					255	
Phe	Gln	Asp	Asp	Asn	Pro	Thr	Asn	Ser	Ser	Glu	Tyr	Asn	Leu	Tyr	Lys
			260					265					270		
Ile	Gly	Gly	Thr	Glu	Lys	Leu	Pro	Tyr	Ala	Val	Ser	Leu	Ile	Gly	Glu
		275					280					285			
Lys	Ile	Phe	Tyr	Pro	Val	Asn	Gly	Gln	Ser	Phe	Thr	Ile	Asn	Asp	Ser
	290					295					300				
Ser	Val	Leu	Glu	Thr	Asn	Trp	Asn	Arg	Val	Thr	Ala	Val	Ala	Met	Pro
305					310					315					320
Glu	Val	Asn	Val	Pro	Val	Leu	Cys	Trp	Pro	Ala	Arg	Leu	Leu	Leu	Asn
				325					330					335	
Ala	Asp	Val	Asn	Ala	Pro	Asp	Ala	Gly	Gln	Tyr	Ser	Gly	Gln	Ile	Tyr
			340					345					350		
Ile	Thr	Phe	Thr	Pro	Ser	Val	Glu	Asn	Leu						
		355					360								

<210> 32

<212> PRT

**<220>**

<400> 32

Ile Ile Asn Phe Ile Arg Lys Tyr Val Tyr Pro Ala Arg Ile Ile Ala  
20 25 30

Ile	Leu	Ala	Gly	Ala	Thr	Leu	Pro	Gln	Val	Ala	Asp	Ala	Ile	Thr	Val
	35						40					45			
Asp	Leu	Asn	Tyr	Asp	Lys	Asn	Asn	Val	Ala	Val	Ile	Thr	Pro	Val	Trp
	50					55					60				
Ser	Gln	Glu	Trp	Ser	Val	Ala	Asn	Val	Leu	Gly	Gly	Trp	Val	Cys	Arg
	65				70					75					80
Ser	Asn	Arg	Asn	Glu	Asn	Glu	Gly	Cys	Glu	Glu	Thr	His	Leu	Val	Trp
			85						90					95	
Trp	Tyr	Ala	Phe	Gly	Ala	Tyr	Ser	Ile	Arg	Leu	Arg	Phe	Arg	Glu	Gln
			100					105					110		
Ile	Ser	His	Ala	Glu	Ile	Thr	Leu	Ile	Leu	Leu	Gly	Ser	Val	Arg	Asp
		115					120					125			
Ala	Cys	Thr	Gly	Val	Ile	Asn	Met	Asn	Ala	Ala	Ala	Cys	Gln	Trp	Gly
	130					135					140				
Arg	Ser	Leu	Lys	Leu	Arg	Ile	Pro	Ser	Glu	Glu	Leu	Ala	Lys	Ile	Pro
	145				150					155					160
Thr	Ser	Gly	Thr	Trp	Lys	Ala	Thr	Leu	Val	Leu	Asp	Tyr	Leu	Gln	Trp
				165					170					175	
Gly	Gly	Asp	Asp	Pro	Leu	Gly	Thr	Ser	Thr	Thr	Asp	Ile	Thr	Leu	Asn
			180					185					190		
Val	Thr	Asp	His	Phe	Ala	Glu	Asn	Ala	Ala	Ile	Tyr	Phe	Pro	Gln	Phe
		195					200					205			
Gly	Thr	Ala	Thr	Pro	Arg	Val	Asp	Leu	Asn	Leu	His	Arg	Met	Asn	Ala
	210					215					220				
Ser	Gln	Met	Ser	Gly	Arg	Ala	Asn	Leu	Asp	Met	Cys	Leu	Tyr	Asp	Gly
	225				230					235					240
Gly	Val	Lys	Ala	Arg	Ser	Leu	Gln	Met	Met	Glu	Gly	Ser	Asn	Lys	Ser
				245					250					255	
Gly	Thr	Gly	Phe	Gln	Val	Ile	Lys	Ser	Asp	Ser	Ala	Asp	Thr	Ile	Asp
			260					265					270		
Tyr	Ala	Val	Ser	Met	Asn	Tyr	Gly	Gly	Arg	Ser	Ile	Pro	Val	Thr	Arg
		275					280					285			
Gly	Val	Glu	Phe	Ser	Leu	Asp	Asn	Val	Asp	Lys	Ala	Ala	Thr	Arg	Pro
	290					295					300				
Val	Val	Leu	Pro	Gly	Gln	Arg	Gln	Ala	Val	Arg	Cys	Val	Pro	Val	Pro
	305				310					315					320
Leu	Thr	Leu	Thr	Thr	Gln	Pro	Phe	Asn	Ile	Arg	Glu	Lys	Arg	Ser	Gly
				325					330					335	
Glu	Tyr	Gln	Gly	Thr	Leu	Thr	Val	Thr	Met	Leu	Met	Gly	Thr	Gln	Thr
			340					345					350		

Pro

<210> 33

<211> 165

<212> PRT

<213> Artificial Sequence

<220>

<223> ETEC Protein Homology Sequence

<400> 33

Met	Lys	Leu	Lys	Lys	Thr	Ile	Gly	Ala	Met	Ala	Leu	Thr	Thr	Met	Phe
1				5					10					15	

Val	Ala	Met	Ser	Ala	Ser	Ala	Val	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
			20					25					30		
Ser	Val	Asp	Pro	Thr	Ile	Asp	Ile	Leu	Gln	Ala	Asp	Gly	Ser	Ser	Leu
		35					40					45			
Pro	Thr	Ala	Val	Glu	Leu	Thr	Tyr	Ser	Pro	Ala	Ala	Ser	Arg	Phe	Glu
		50				55						60			
Asn	Tyr	Lys	Ile	Ala	Thr	Lys	Val	His	Thr	Asn	Val	Ile	Asn	Lys	Asn
65					70					75					80
Val	Leu	Val	Lys	Leu	Val	Asn	Asp	Pro	Lys	Leu	Thr	Asn	Val	Leu	Asp
			85						90					95	
Ser	Thr	Lys	Gln	Leu	Pro	Ile	Thr	Val	Ser	Tyr	Gly	Gly	Lys	Leu	Ser
			100					105					110		
Thr	Ala	Asp	Val	Thr	Phe	Glu	Pro	Ala	Glu	Leu	Asn	Phe	Gly	Thr	Ser
		115					120					125			
Gly	Val	Thr	Gly	Val	Ser	Ser	Ser	Gln	Asp	Leu	Val	Ile	Gly	Ala	Thr
		130				135					140				
Thr	Ala	Gln	Ala	Pro	Ser	Ala	Asn	Tyr	Ser	Gly	Val	Val	Ser	Ile	Leu
145					150					155					160
Met	Thr	Leu	Ala	Ser											
				165											

<210> 34

<211> 168

<212> PRT

<213> Artificial Sequence

<220>

<223> ETEC Protein Homology Sequence

<400> 34

Met	Lys	Phe	Lys	Lys	Thr	Ile	Gly	Ala	Met	Ala	Leu	Thr	Thr	Met	Phe
1				5					10					15	
Val	Ala	Val	Ser	Ala	Ser	Ala	Val	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
			20					25					30		
Ser	Val	Asp	Pro	Ala	Ile	Asp	Leu	Gln	Ala	Asp	Gly	Asn	Ala	Leu	
		35					40				45				
Pro	Ser	Val	Lys	Leu	Ala	Tyr	Ser	Pro	Ala	Ser	Lys	Ile	Phe	Glu	Ser
		50				55					60				
Tyr	Arg	Val	Met	Thr	Gln	Val	His	Thr	Asn	Asp	Ala	Thr	Lys	Lys	Val
65					70					75					80
Ile	Val	Lys	Leu	Ala	Asp	Thr	Pro	Gln	Leu	Thr	Asp	Val	Leu	Asn	Ser
			85						90					95	
Thr	Val	Gln	Met	Pro	Ile	Ser	Val	Ser	Trp	Gly	Gly	Val	Leu	Ser	Thr
			100					105					110		
Thr	Ala	Lys	Glu	Phe	Glu	Ala	Ala	Ala	Leu	Gly	Tyr	Ser	Ala	Ser	Gly
		115					120					125			
Val	Asn	Gly	Val	Ser	Ser	Ser	Ser	Gln	Glu	Leu	Val	Ile	Ser	Ala	Pro
		130				135					140				
Lys	Thr	Ala	Gly	Thr	Ala	Pro	Thr	Ala	Gly	Asn	Tyr	Ser	Gly	Val	Val
145					150					155					160
Ser	Leu	Val	Met	Thr	Leu	Gly	Ser								
				165											

<210> 35  
 <211> 170  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ETEC Protein Homology Sequence

<400> 35  
 Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ala Thr Leu Phe  
 1 5 10 15  
 Ala Thr Met Gly Ala Ser Ala Val Glu Lys Thr Ile Ser Val Thr Ala  
 20 25 30  
 Ser Val Asp Pro Thr Val Asp Leu Leu Gln Ser Asp Gly Ser Ala Leu  
 35 40 45  
 Pro Asn Val Ala Leu Thr Tyr Ser Pro Ala Val Asn Asn Phe Glu Ala  
 50 55 60  
 His Thr Ile Asn Thr Val Val His Thr Asn Asp Ser Asp Lys Gly Val  
 65 70 75 80  
 Val Val Lys Leu Ser Ala Asp Pro Val Leu Ser Asn Val Leu Asn Pro  
 85 90 95  
 Thr Leu Gln Ile Pro Val Ser Val Asn Phe Ala Gly Lys Pro Leu Ser  
 100 105 110  
 Thr Thr Gly Ile Thr Ile Asp Ser Asn Asp Leu Asn Phe Ala Ser Ser  
 115 120 125  
 Gly Val Asn Tyr Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala Asp  
 130 135 140  
 Ala Thr Arg Val Thr Gly Gly Ala Leu Thr Ala Gly Gln Tyr Gln Gly  
 145 150 155 160  
 Leu Val Ser Ile Ile Leu Thr Lys Ser Thr  
 165 170

<210> 36  
 <211> 170  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ETEC Protein Homology Sequence

<400> 36  
 Met Lys Leu Asn Lys Ile Ile Gly Ala Leu Val Leu Ser Ser Thr Phe  
 1 5 10 15  
 Val Ser Met Gly Ala Ser Ala Ala Glu Lys Asn Ile Thr Val Thr Ala  
 20 25 30  
 Ser Val Asp Pro Thr Ile Asp Leu Met Gln Ser Asp Gly Thr Ala Leu  
 35 40 45  
 Pro Ser Ala Val Asn Ile Ala Tyr Leu Pro Gly Glu Lys Arg Phe Glu  
 50 55 60  
 Ser Ala Arg Ile Asn Thr Gln Val His Thr Asn Asn Lys Thr Lys Gly  
 65 70 75 80  
 Ile Gln Ile Lys Leu Thr Asn Asp Asn Val Val Met Thr Asn Leu Ser  
 85 90 95  
 Asp Pro Ser Lys Thr Ile Pro Leu Glu Val Ser Phe Ala Gly Thr Lys

	100		105		110										
Leu	Ser	Thr	Ala	Ala	Thr	Ser	Ile	Thr	Ala	Asp	Gln	Leu	Asn	Phe	Gly
	115						120					125			
Ala	Ala	Gly	Val	Glu	Thr	Val	Ser	Ala	Thr	Lys	Glu	Leu	Val	Ile	Asn
	130						135					140			
Ala	Gly	Ser	Thr	Gln	Gln	Thr	Asn	Ile	Val	Ala	Gly	Asn	Tyr	Gln	Gly
145				150						155					160
Leu	Val	Ser	Ile	Val	Leu	Thr	Gln	Glu	Pro						
			165						170						

<210> 37  
 <211> 168  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ETEC Protein Homology Sequence

<400> 37															
Met	Lys	Leu	Lys	Tyr	Thr	Ile	Gly	Ala	Met	Ala	Leu	Ser	Thr	Ile	Phe
1			5					10						15	
Val	Ala	Val	Ser	Ala	Ser	Ala	Val	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
			20					25					30		
Ser	Val	Asp	Pro	Thr	Ile	Asp	Ile	Leu	Gln	Ala	Asn	Gly	Ser	Ala	Leu
		35					40					45			
Pro	Thr	Ala	Val	Asp	Leu	Thr	Tyr	Leu	Pro	Gly	Ala	Lys	Thr	Phe	Glu
	50					55					60				
Asn	Tyr	Ser	Val	Leu	Thr	Gln	Ile	Tyr	Thr	Asn	Asp	Pro	Ser	Lys	Gly
65				70						75				80	
Leu	Asp	Val	Arg	Leu	Val	Asp	Thr	Pro	Lys	Leu	Thr	Asn	Ile	Leu	Gln
			85					90					95		
Pro	Thr	Ser	Thr	Ile	Pro	Leu	Thr	Val	Ser	Trp	Ala	Gly	Arg	Thr	Leu
		100						105					110		
Ser	Thr	Ser	Ala	Gln	Lys	Ile	Ala	Val	Gly	Asp	Leu	Gly	Phe	Gly	Ser
		115					120					125			
Thr	Gly	Thr	Ala	Gly	Val	Ser	Asn	Ser	Lys	Glu	Leu	Val	Ile	Gly	Ala
	130					135					140				
Thr	Thr	Ser	Gly	Lys	Pro	Ser	Ala	Gly	Lys	Tyr	Gln	Gly	Val	Val	Ser
145				150						155					160
Ile	Val	Met	Thr	Gln	Ser	Thr	Asn								
				165											

<210> 38  
 <211> 142  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> ETEC Protein Homology Sequence

<400> 38															
Val	Asp	Pro	Thr	Ile	Asp	Ile	Leu	Gln	Ala	Asn	Gly	Ser	Ala	Leu	Pro
1				5				10						15	

Thr Ala Val Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn  
 20 25 30  
 Tyr Ser Val Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu  
 35 40 45  
 Asp Val Arg Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro  
 50 55 60  
 Thr Ser Thr Ile Pro Leu Thr Val Ser Trp Ala Gly Lys Thr Leu Ser  
 65 70 75 80  
 Thr Ser Ala Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser Thr  
 85 90 95  
 Gly Thr Ala Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala Thr  
 100 105 110  
 Thr Ser Gly Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val Ser  
 115 120 125  
 Ile Val Met Thr Gln Ser Thr Asp Thr Ala Ala Pro Val Pro  
 130 135 140

<210> 39

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> ETEC Protein Homology Sequence

<400> 39

Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro  
 1 5 10 15  
 Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val  
 20 25 30  
 Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Thr Lys Ala Val  
 35 40 45  
 Val Val Lys Leu Ser Ala Pro Ala Val Leu Ser Asn Ile Met Lys Pro  
 50 55 60  
 Ser Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Lys Thr Leu Ser  
 65 70 75 80  
 Thr Ala Asp Ala Glu Phe Ala Ala Asp Thr Leu Asn Phe Gly Ala Ser  
 85 90 95  
 Gly Val Glu Asn Val Ser Ser Val Gln Gln Leu Thr Ile His Ala Glu  
 100 105 110  
 Ala Ala Pro Pro Glu Ala Gly Asn Tyr Gln Gly Val Ile Ser Leu Ile  
 115 120 125  
 Met Thr Gln Lys Thr  
 130

<210> 40

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> ETEC Protein Homology Sequence

<400> 40

Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro  
1 5 10 15  
Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val  
20 25 30  
Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Ser Lys Gly Val  
35 40 45  
Val Val Lys Leu Ser Ala Ser Pro Val Leu Ser Asn Ile Met Pro Asn  
50 55 60  
Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Glu Thr Leu Asn Thr  
65 70 75 80  
Thr Asp Thr Glu Phe Thr Val Asp Thr Leu Asn Phe Gly Thr Ser Gly  
85 90 95  
Val Glu Asn Val Ser Ser Thr Gln Gln Leu Thr Ile His Ala Asp Thr  
100 105 110  
Gln Gly Thr Ala Pro Glu Ala Gly Asn Tyr Gln Gly Ile Ile Ser Leu  
115 120 125  
Ile Met Thr Gln Lys Thr  
130

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